WHAT IS CLAIMED IS:

1. An isolated nucleic acid encoding a polypeptide comprising amino acid residues 11-140 of SEQ ID NO:1, or amino acid residues 11-140 of SEQ ID NO:1 with a conservative amino acid substitution.

2. The isolated nucleic acid of Claim 1 further comprising a heterologous nucleotide sequence.

3. An isolated nucleic acid encoding a peptide derived from FGFR1 consisting of 16 to 50 amino acids comprising the amino acid sequence of SEQ ID NO:5:

Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val;

wherein said peptide binds to the PTB domain of SNT1.

4. The isolated nucleic acid of Claim 3 further comprising a heterologous nucleotide sequence.

5. An isolated nucleic acid encoding a peptide derived from FGFR1 consisting of 16 to 50 amino acids comprising the amino acid sequence of SEQ ID NO:3 or SEQ ID NO:3 with a conservative amino acid substitution; wherein the peptide can bind to the PTB domain of SNT1.

6. The isolated nucleic acid of Claim 5 further comprising a heterologous nucleotide sequence.

7. A polypeptide comprising the amino acid residues 11-140 of SEQ ID NO:1, or amino acid residues 11-140 of SEQ ID NO:1 with a conservative amino acid substitution.

8. A fusion protein or peptide comprising the polypeptide of Claim 7.

9. An isolated peptide derived from FGFR1 consisting of 16 to 50 amino acids comprising the amino acid sequence of SEQ ID NO:5:

Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val;

wherein the peptide can bind to the PTB domain of SNT1.

10. A fusion protein or peptide comprising the peptide of Claim 9.

11. An isolated peptide derived from FGFR1 consisting of 16 to 50 amino acids comprising the amino acid sequence of SEQ ID NO:3 or SEQ ID NO:3 with a conservative amino acid substitution; wherein said peptide can bind to the PTB domain of SNT1.

12. A fusion protein or peptide comprising the peptide of Claim 11.

13. A method of identifying a compound that stabilizes a SNT/FGFR complex using the three-dimensional structure of the SNT/FGFR complex comprising:

(a) selecting a potential compound by performing rational drug design with the set of atomic coordinates obtained from Tables 1-5, wherein said selecting is performed in conjunction with computer modeling;

(b) contacting the potential compound with a SNT/FGFR complex comprising an SNT or an SNT fragment, and FGFR or an FGFR fragment; and

(c) measuring the stability of the SNT/FGFR complex; wherein a potential compound is identified as a compound that stabilizes the SNT/FGFR complex when there is an increase in the stability of the SNT/FGFR complex.

14. A method of identifying a compound that destabilizes a SNT/FGFR complex using the three-dimensional structure of the SNT/FGFR complex comprising:

(a) selecting a potential compound by performing rational drug design with the set of atomic coordinates obtained from Tables 1-5, wherein said selecting is performed in conjunction with computer modeling;

(b) contacting the potential compound with a SNT/FGFR complex comprising an SNT or an SNT fragment, and FGFR or an FGFR fragment; and

(c) measuring the stability of the SNT/FGFR complex; wherein a potential compound is identified as a compound that destabilizes the SNT/FGFR complex when there is a decrease in the stability of the SNT/FGFR complex.

15. A method of identifying a compound that inhibits the formation of a SNT/FGFR complex using the three-dimensional structure of the SNT/FGFR complex comprising:

(a) selecting a potential compound that binds to the PTB domain of SNT; wherein said selecting is performed using rational drug design with the set of atomic coordinates obtained from Tables 1-5, and is performed in conjunction with computer modeling;

(b) contacting the potential compound with an SNT or an SNT fragment, and FGFR or an FGFR fragment under conditions in which the SNT/FGFR complex can form in the absence of the potential compound; and

(c) measuring the binding affinity of the SNT or the SNT fragment with FGFR or the FGFR fragment; wherein a potential compound is identified as a compound that inhibits the formation of the SNT/FGFR complex when there is a decrease in the binding affinity of the SNT or the SNT fragment with FGFR or the FGFR fragment.

16. A method of identifying a compound that stabilizes a SNT/FGFR complex comprising:

(a) obtaining a set of atomic coordinates defining the three-dimensional structure of a SNT/FGFR complex consisting of a fragment of SNT consisting of amino acid residues 11-140 of SEQ ID NO:1 and a fragment of FGFR consisting of SEQ ID NO:3;

(b) selecting a potential compound by performing rational drug design with the atomic coordinates obtained in step (a), wherein said selecting is performed in conjunction with computer modeling;

(c) contacting the potential compound with a SNT/FGFR complex; wherein said SNT/FGFR complex comprises an SNT or an SNT fragment, and FGFR or an FGFR fragment; and

(d) measuring the stability of the SNT/FGFR complex of step (c); wherein a potential compound is identified as a compound that stabilizes the SNT/FGFR complex when there is an increase in the stability of the SNT/FGFR complex of step (c).

17. A method of identifying a compound that destabilizes a SNT/FGFR complex comprising:

(a) obtaining a set of atomic coordinates defining the three-dimensional structure of a SNT/FGFR complex consisting of a fragment of SNT consisting of amino acid residues 11-140 of SEQ ID NO:1 and a fragment of FGFR consisting of SEQ ID NO:3;

(b) selecting a potential compound by performing rational drug design with the atomic coordinates obtained in step (a), wherein said selecting is performed in conjunction with computer modeling;

(c) contacting the potential compound with a SNT/FGFR complex; wherein said SNT/FGFR complex comprises an SNT or an SNT fragment, and FGFR or an FGFR fragment; and

(d) measuring the stability of the SNT/FGFR complex of step (c); wherein a potential compound is identified as a compound that stabilizes the SNT/FGFR complex when there is a decrease in the stability of the SNT/FGFR complex of step (c).

18. A method of identifying a compound that inhibits the formation of a SNT/FGFR complex using the three-dimensional structure of the SNT/FGFR complex comprising: comprising:

(a) obtaining a set of atomic coordinates defining the three-dimensional structure of a SNT/FGFR complex consisting of a fragment of SNT consisting of amino acid residues 11-140 of SEQ ID NO:1 and a fragment of FGFR consisting of SEQ ID NO:3;

(b) selecting a potential compound that binds to the PTB domain of SNT; wherein said selecting is performed using rational drug design with the set of atomic coordinates obtained from step (a), and is performed in conjunction with computer

modeling; ;

(c) contacting the potential compound with an SNT or an SNT fragment, and FGFR or an FGFR fragment under conditions in which the SNT/FGFR complex can form in the absence of the potential compound; and

(d) measuring the binding affinity of the SNT or the SNT fragment with FGFR or the FGFR fragment; wherein a potential compound is identified as a compound that inhibits the formation of the SNT/FGFR complex when there is a decrease in the binding affinity of the SNT or the SNT fragment with FGFR or the FGFR fragment.

19. A method of selecting a compound that potentially inhibits the SNT/FGFR dependent cellular signaling pathway comprising:

(a) defining the structure of the SNT/FGFR complex by the atomic coordinates obtained from Tables 1-5; and

(b) selecting a compound which potentially inhibits the SNT/FGFR dependent cellular signaling pathway; wherein said selecting is performed with the aid of the structure defined in step (a).

20. A method of selecting a compound that potentially stimulates the SNT/FGFR dependent cellular signaling pathway comprising:

(a) defining the structure of the SNT/FGFR complex by the atomic coordinates obtained from Tables 1-5; and

(b) selecting a compound which potentially stimulates the SNT/FGFR dependent cellular signaling pathway; wherein said selecting is performed with the aid of the structure defined in step (a).

21. A method of selecting a compound that potentially binds to the PTB domain of SNT1 or the SNT/FGFR complex comprising:

(a) defining the structure of the SNT/FGFR complex by the atomic coordinates obtained from Tables 1-5; and

(b) selecting a compound which potentially binds the PTB domain of SNT1 or the SNT/FGFR complex; wherein said selecting is performed with the aid of the structure defined in step (a).

22. A computer comprising a representation of a SNT/FGFR complex in computer memory which comprises:

(a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises structural coordinates from Tables 1-5;

(b) a working memory for storing instructions for processing said machine-readable data;

(c) a central processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine readable data into a three-dimensional representation of the SNT/FGFR complex; and

(d) a display coupled to said central-processing unit for displaying said three-dimensional representation.